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1643

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/428,122

DATE: 02/24/2000
TIME: 16:25:32

Input Set: I428122.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Connaught Laboratories Limited
2 Murdin et al.
3 <120> TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
4 USES THEREOF
5 <130> FILE REFERENCE: 19721-007-019
6 <140> CURRENT APPLICATION NUMBER: US/09/428,122
7 <141> CURRENT FILING DATE: 1999-10-27
8 <150> EARLIER APPLICATION NUMBER: 60/106,046
9 <151> EARLIER FILING DATE: 1998-10-28
10 <150> EARLIER APPLICATION NUMBER: 60/132,271
11 <151> EARLIER FILING DATE: 1999-05-03
12 <160> NUMBER OF SEQ ID NOS: 4
13 <170> SOFTWARE: PatentIn Ver. 2.0
14 <210> SEQ ID NO 1
15 <211> LENGTH: 3000
16 <212> TYPE: DNA
17 <213> ORGANISM: Chlamydia pneumoniae
18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (101)..(2884)
21 <400> SEQUENCE: 1
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23 cttaaaatataaaattcaaa atcaaagtat atattttaca atg aag tct tct ttc 115
24 Met Lys Ser Ser Phe
25 1 5
26 ccc aag ttt gta ttt tct aca ttt gct att ttc cct ttg tct atg att 163
27 Pro Lys Phe Val Phe Ser Thr Phe Ala Ile Phe Pro Leu Ser Met Ile
28 10 15 20
29 gct acc gag aca gtt ttg gat tca agt gcg agt ttc gat ggg aat aaa 211
30 Ala Thr Glu Thr Val Leu Asp Ser Ser Ala Ser Phe Asp Gly Asn Lys
31 25 30 35
32 aat ggt aat ttt tca gtt cgt gag agt cag gaa gat gct gga act acc 259
33 Asn Gly Asn Phe Ser Val Arg Glu Ser Gln Glu Asp Ala Gly Thr Thr
34 40 45 50
35 tac cta ttt aag gga aat gtc act cta gaa aat att cct gga aca ggc 307
36 Tyr Leu Phe Lys Gly Asn Val Thr Leu Glu Asn Ile Pro Gly Thr Gly
37 55 60 65
38 aca gca atc aca aaa agc tgt ttt aac aac act aag ggc gat ttg act 355
39 Thr Ala Ile Thr Lys Ser Cys Phe Asn Asn Thr Lys Gly Asp Leu Thr
40 70 75 80 85
41 ttc aca ggt aac ggg aac tct cta ttg ttc caa acg gtg gat gca ggg 403
42 Phe Thr Gly Asn Gly Asn Ser Leu Leu Phe Gln Thr Val Asp Ala Gly
43 90 95 100
44 act gta gca ggg gct gct gtt aac aac agc agc gtg gta gat aaa tct acc 451

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47	acg ttt ata ggg ttt tct tcg cta tct ttt att gcg tct cct gga agt	499		
48	Thr Phe Ile Gly Phe Ser Ser Leu Ser Phe Ile Ala Ser Pro Gly Ser			
49	120	125	130	
50	tcg ata act acc ggc aaa gga gcc gtt agc tgc tct acg ggt agc ttg	547		
51	Ser Ile Thr Thr Gly Lys Gly Ala Val Ser Cys Ser Thr Gly Ser Leu			
52	135	140	145	
53	agt ttg aca aaa aat gtc agt ttg ctc ttc agc aaa aac ttt tca acg	595		
54	Ser Leu Thr Lys Asn Val Ser Leu Leu Phe Ser Lys Asn Phe Ser Thr			
55	150	155	160	165
56	gat aat ggc ggt gct atc acc gca aaa act ctt tca tta aca ggg act	643		
57	Asp Asn Gly Gly Ala Ile Thr Ala Lys Thr Leu Ser Leu Thr Gly Thr			
58	170	175	180	
59	aca atg tca gct ctg ttt tct gaa aat acc tcc tca aag aaa ggc gga	691		
60	Thr Met Ser Ala Leu Phe Ser Glu Asn Thr Ser Ser Lys Lys Gly Gly			
61	185	190	195	
62	gcc att cag act tcc gat gcc ctt acc att act gga aac caa ggg gaa	739		
63	Ala Ile Gln Thr Ser Asp Ala Leu Thr Ile Thr Gly Asn Gln Gly Glu			
64	200	205	210	
65	gtc tct ttt tct gac aat act tct tcg gat tct gga gct gca att ttt	787		
66	Val Ser Phe Ser Asp Asn Thr Ser Ser Asp Ser Gly Ala Ala Ile Phe			
67	215	220	225	
68	aca gaa gcc tcg gtg act att tct aat aat gct aaa gtt tcc ttt att	835		
69	Thr Glu Ala Ser Val Thr Ile Ser Asn Asn Ala Lys Val Ser Phe Ile			
70	230	235	240	245
71	gac aat aag gtc aca gga gcg agc tcc tca aca acg ggg gat atg tca	883		
72	Asp Asn Lys Val Thr Gly Ala Ser Ser Thr Thr Gly Asp Met Ser			
73	250	255	260	
74	gga ggt gct atc tgt gct tat aaa act agt aca gat act aag gtc acc	931		
75	Gly Gly Ala Ile Cys Ala Tyr Lys Thr Ser Thr Asp Thr Lys Val Thr			
76	265	270	275	
77	ctc act gga aat cag atg tta ctc ttc agc aac aat aca tcg aca aca	979		
78	Leu Thr Gly Asn Gln Met Leu Leu Phe Ser Asn Asn Thr Ser Thr Thr			
79	280	285	290	
80	gcg gga gga gct atc tat gtg aaa aag ctc gaa ctg gct tcc gga gga	1027		
81	Ala Gly Gly Ala Ile Tyr Val Lys Lys Leu Glu Leu Ala Ser Gly Gly			
82	295	300	305	
83	ctt acc cta ttc agt aga aat agt gtc aat gga ggt aca gct cct aaa	1075		
84	Leu Thr Leu Phe Ser Arg Asn Ser Val Asn Gly Gly Thr Ala Pro Lys			
85	310	315	320	325
86	ggt gga gcc ata gct atc gaa gat agt ggg gaa ttg agt tta tcc gcc	1123		
87	Gly Gly Ala Ile Ala Ile Glu Asp Ser Gly Glu Leu Ser Leu Ser Ala			
88	330	335	340	
89	gat agt ggt gac att gtc ttt tta ggg aat aca gtc act tct act act	1171		
90	Asp Ser Gly Asp Ile Val Phe Leu Gly Asn Thr Val Thr Ser Thr Thr			
91	345	350	355	
92	cct ggg acg aat aga agt agt atc gac tta gga acg agt gca aag atg	1219		
93	Pro Gly Thr Asn Arg Ser Ser Ile Asp Leu Gly Thr Ser Ala Lys Met			
94	360	365	370	

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95	aca gct ttg cgt tct gct ggt aga gcc atc tac ttc tat gat ccc	1267
96	Thr Ala Leu Arg Ser Ala Ala Gly Arg Ala Ile Tyr Phe Tyr Asp Pro	
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98	ata act aca gga tca tcc aca aca gtt aca gat gtc tta aaa gtt aat	1315
99	Ile Thr Thr Gly Ser Ser Thr Thr Val Thr Asp Val Leu Lys Val Asn	
100	390 395 400 405	
101	gag act ccg gca gat tct gca cta caa tat aca ggg aac atc atc ttc	1363
102	Glu Thr Pro Ala Asp Ser Ala Leu Gln Tyr Thr Gly Asn Ile Ile Phe	
103	410 415 420	
104	aca gga gaa aag tta tca gag aca gag gcc gca gat tct aaa aat ctt	1411
105	Thr Gly Glu Lys Leu Ser Glu Thr Glu Ala Ala Asp Ser Lys Asn Leu	
106	425 430 435	
107	act tcg aag cta cta cag cct gta act ctt tca gga ggt act cta tct	1459
108	Thr Ser Lys Leu Leu Gln Pro Val Thr Leu Ser Gly Gly Thr Leu Ser	
109	440 445 450	
110	tta aaa cat gga gtg act ctg cag act cag gca ttc act caa cag gca	1507
111	Leu Lys His Gly Val Thr Leu Gln Thr Gln Ala Phe Thr Gln Gln Ala	
112	455 460 465	
113	gat tct cgt ctc gaa atg gac gta gga act act cta gaa cct gct gat	1555
114	Asp Ser Arg Leu Glu Met Asp Val Gly Thr Thr Leu Glu Pro Ala Asp	
115	470 475 480 485	
116	act agc acc ata aac aat ttg gtc att aac atc agt tct ata gac ggt	1603
117	Thr Ser Thr Ile Asn Asn Leu Val Ile Asn Ile Ser Ser Ile Asp Gly	
118	490 495 500	
119	gca aag aag gca aaa ata gaa acc aaa gct acg tca aaa aat ctg act	1651
120	Ala Lys Lys Ala Lys Ile Glu Thr Lys Ala Thr Ser Lys Asn Leu Thr	
121	505 510 515	
122	tta tct gga acc atc act tta ttg gac ccg acg ggc acg ttt tat gaa	1699
123	Leu Ser Gly Thr Ile Thr Leu Leu Asp Pro Thr Gly Thr Phe Tyr Glu	
124	520 525 530	
125	aat cat agt tta aga aat cct cag tcc tac gac atc tta gag ctc aaa	1747
126	Asn His Ser Leu Arg Asn Pro Gln Ser Tyr Asp Ile Leu Glu Leu Lys	
127	535 540 545	
128	gct tct gga act gta aca agc acc gca gtg act cca gat cct ata atg	1795
129	Ala Ser Gly Thr Val Thr Ser Thr Ala Val Thr Pro Asp Pro Ile Met	
130	550 555 560 565	
131	ggt gag aaa ttc cat tac ggc tat cag gga act tgg ggc cca att gtt	1843
132	Gly Glu Lys Phe His Tyr Gly Tyr Gln Gly Thr Trp Gly Pro Ile Val	
133	570 575 580	
134	tgg ggg aca ggg gct tct acg act gca acc ttc aac tgg act aaa act	1891
135	Trp Gly Thr Gly Ala Ser Thr Thr Ala Thr Phe Asn Trp Thr Lys Thr	
136	585 590 595	
137	ggc tat att cct aat ccc gag cgt atc ggc tct tta gtc cct aat agc	1939
138	Gly Tyr Ile Pro Asn Pro Glu Arg Ile Gly Ser Leu Val Pro Asn Ser	
139	600 605 610	
140	tta tgg aat gca ttt ata gat att agc tct ctc cat tat ctt atg gag	1987
141	Leu Trp Asn Ala Phe Ile Asp Ile Ser Ser Leu His Tyr Leu Met Glu	
142	615 620 625	
143	act gca aac gaa ggg ttg cag gga gac cgt gct ttt tgg tgt gct gga	2035
144	Thr Ala Asn Glu Gly Leu Gln Gly Asp Arg Ala Phe Trp Cys Ala Gly	

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145	630	635	640	645
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149	cgc cat ttg agt ggc ggt tat gtc ata gga gga aac cta cat act tgt			2131
150	Arg His Leu Ser Gly Gly Tyr Val Ile Gly Gly Asn Leu His Thr Cys			
151	665	670	675	
152	tca gat aag att ctt agt gct gca ttt tgt cag ctc ttt gga aga gat			2179
153	Ser Asp Lys Ile Leu Ser Ala Ala Phe Cys Gln Leu Phe Gly Arg Asp			
154	680	685	690	
155	aga gac tac ttt gta gct aag aat caa ggt aca gtc tac gga gga act			2227
156	Arg Asp Tyr Phe Val Ala Lys Asn Gln Gly Thr Val Tyr Gly Thr			
157	695	700	705	
158	ctc tat tac cag cac aac gaa acc tat atc tct ctt cct tgc aaa cta			2275
159	Leu Tyr Tyr Gln His Asn Glu Thr Tyr Ile Ser Leu Pro Cys Lys Leu			
160	710	715	720	725
161	cgg cct tgt tcg ttg tct tat gtt cct aca gag att cct gtt ctc ttt			2323
162	Arg Pro Cys Ser Leu Ser Tyr Val Pro Thr Glu Ile Pro Val Leu Phe			
163	730	735	740	
164	tca gga aac ctt agc tac acc cat acg gat aac gat ctg aaa acc aag			2371
165	Ser Gly Asn Leu Ser Tyr Thr His Thr Asp Asn Asp Leu Lys Thr Lys			
166	745	750	755	
167	tat aca aca tat cct act gtt aaa gga agc tgg ggg aat gat agt ttc			2419
168	Tyr Thr Tyr Pro Thr Val Lys Gly Ser Trp Gly Asn Asp Ser Phe			
169	760	765	770	
170	gct tta gaa ttc ggt gga aga gct ccg att tgc tta gat gaa agt gct			2467
171	Ala Leu Glu Phe Gly Gly Arg Ala Pro Ile Cys Leu Asp Glu Ser Ala			
172	775	780	785	
173	cta ttt gag cag tac atg ccc ttc atg aaa ttg cag ttt gtc tat gca			2515
174	Leu Phe Glu Gln Tyr Met Pro Phe Met Lys Leu Gln Phe Val Tyr Ala			
175	790	795	800	805
176	cat cag gaa ggt ttt aaa gaa cag gga aca gaa gct cgt gaa ttt gga			2563
177	His Gln Glu Gly Phe Lys Glu Gln Gly Thr Glu Ala Arg Glu Phe Gly			
178	810	815	820	
179	agt agc cgt ctt gtg aat ctt gcc tta cct atc ggg atc cga ttt gat			2611
180	Ser Ser Arg Leu Val Asn Leu Ala Leu Pro Ile Gly Ile Arg Phe Asp			
181	825	830	835	
182	aag gaa tca gac tgc caa gat gca acg tac aat cta act ctt ggt tat			2659
183	Lys Glu Ser Asp Cys Gln Asp Ala Thr Tyr Asn Leu Thr Leu Gly Tyr			
184	840	845	850	
185	act gtg gat ctt gtt cgt agt aac ccc gac tgc acg aca aca ctg cga			2707
186	Thr Val Asp Leu Val Arg Ser Asn Pro Asp Cys Thr Thr Thr Leu Arg			
187	855	860	865	
188	att agc ggt gat tct tgg aaa acc ttc ggt acg aat ttg gca aga caa			2755
189	Ile Ser Gly Asp Ser Trp Lys Thr Phe Gly Thr Asn Leu Ala Arg Gln			
190	870	875	880	885
191	gct tta gtc ctt cgt gca ggg aac cat ttt tgc ttt aac tca aat ttt			2803
192	Ala Leu Val Leu Arg Ala Gly Asn His Phe Cys Phe Asn Ser Asn Phe			
193	890	895	900	
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 198 Tyr Asn Val Asp Leu Gly Ala Lys Tyr Gln Phe
 199 920 925
 200 agagctccat acatcgaagg gaaaagagct tttaagattt cttgaaggct cttttcgatt 2964
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 203 <211> LENGTH: 928
 204 <212> TYPE: PRT
 205 <213> ORGANISM: Chlamydia pneumoniae
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 211 Phe Asp Gly Asn Lys Asn Gly Asn Phe Ser Val Arg Glu Ser Gln Glu
 212 35 40 45
 213 Asp Ala Gly Thr Thr Tyr Leu Phe Lys Gly Asn Val Thr Leu Glu Asn
 214 50 55 60
 215 Ile Pro Gly Thr Gly Thr Ala Ile Thr Lys Ser Cys Phe Asn Asn Thr
 216 65 70 75 80
 217 Lys Gly Asp Leu Thr Phe Thr Gly Asn Gly Asn Ser Leu Leu Phe Gln
 218 85 90 95
 219 Thr Val Asp Ala Gly Thr Val Ala Gly Ala Ala Val Asn Ser Ser Val
 220 100 105 110
 221 Val Asp Lys Ser Thr Thr Phe Ile Gly Phe Ser Ser Leu Ser Phe Ile
 222 115 120 125
 223 Ala Ser Pro Gly Ser Ser Ile Thr Thr Gly Lys Gly Ala Val Ser Cys
 224 130 135 140
 225 Ser Thr Gly Ser Leu Ser Leu Thr Lys Asn Val Ser Leu Leu Phe Ser
 226 145 150 155 160
 227 Lys Asn Phe Ser Thr Asp Asn Gly Gly Ala Ile Thr Ala Lys Thr Leu
 228 165 170 175
 229 Ser Leu Thr Gly Thr Thr Met Ser Ala Leu Phe Ser Glu Asn Thr Ser
 230 180 185 190
 231 Ser Lys Lys Gly Gly Ala Ile Gln Thr Ser Asp Ala Leu Thr Ile Thr
 232 195 200 205
 233 Gly Asn Gln Gly Glu Val Ser Phe Ser Asp Asn Thr Ser Ser Asp Ser
 234 210 215 220
 235 Gly Ala Ala Ile Phe Thr Glu Ala Ser Val Thr Ile Ser Asn Asn Ala
 236 225 230 235 240
 237 Lys Val Ser Phe Ile Asp Asn Lys Val Thr Gly Ala Ser Ser Ser Thr
 238 245 250 255
 239 Thr Gly Asp Met Ser Gly Gly Ala Ile Cys Ala Tyr Lys Thr Ser Thr
 240 260 265 270
 241 Asp Thr Lys Val Thr Leu Thr Gly Asn Gln Met Leu Leu Phe Ser Asn
 242 275 280 285
 243 Asn Thr Ser Thr Thr Ala Gly Gly Ala Ile Tyr Val Lys Lys Leu Glu
 244 290 295 300

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